



#7

1

## SEQUENCE LISTING

<110> CHAMBERLAIN, PIERRE  
METZGER, DANIEL

<120> TRANSGENIC MOUSE FOR TARGETED RECOMBINATION  
MEDIATED BY MODIFIED CRE-ER

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<140> 09/853,033

<141> 2001-05-11

<150> FR 00/12570

<151> 2000-10-03

<160> 14

<170> PatentIn Ver. 2.1

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<211> 1788

<212> DNA

<213> Homo sapiens

<220>

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<222> (1)..(1788)

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Phe Pro Pro Leu Asn Ser Val Ser Pro Ser Pro Leu Met Leu Leu His  
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Homosapiens-Bacteriophage P1

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 Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly  
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<210>	5
<211>	1983
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<222> (1) .. (1983)

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<223> Description of Artificial Sequence: Chimeric sequence  
Homosapiens-Bacteriophage P1

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tca	act	cgc	gcc	ctg	gaa	ggg	att	ttt	gaa	gca	act	cat	cga	ttg	att	816
Ser	Thr	Arg	Ala	Leu	Glu	Gly	Ile	Phe	Glu	Ala	Thr	His	Arg	Leu	Ile	
260265270																
tac	ggc	gct	aag	gat	gac	tct	ggt	cag	aga	tac	ctg	gcc	tgg	tct	gga	864
Tyr	Gly	Ala	Lys	Asp	Asp	Ser	Gly	Gln	Arg	Tyr	Leu	Ala	Trp	Ser	Gly	
275280285																
cac	agt	gcc	cgt	gtc	gga	gcc	gcg	cga	gat	atg	gcc	cgc	gct	gga	gtt	912
His	Ser	Ala	Arg	Val	Gly	Ala	Ala	Arg	Asp	Met	Ala	Arg	Ala	Gly	Val	
290295300																
tca	ata	ccg	gag	atc	atg	caa	gct	ggt	ggc	tgg	acc	aat	gta	aat	att	960
Ser	Ile	Pro	Glu	Ile	Met	Gln	Ala	Gly	Gly	Trp	Thr	Asn	Val	Asn	Ile	
305310315320																
gtc	atg	aac	tat	atc	cgt	aac	ctg	gat	agt	gaa	aca	ggg	gca	atg	gtg	1008
Val	Met	Asn	Tyr	Ile	Arg	Asn	Leu	Asp	Ser	Glu	Thr	Gly	Ala	Met	Val	
325330335																
cgc	ctg	ctg	gaa	gat	ggc	gat	ctc	gag	cca	tct	gct	gga	gac	atg	aga	1056
Arg	Leu	Leu	Glu	Asp	Gly	Asp	Leu	Glu	Pro	Ser	Ala	Gly	Asp	Met	Arg	
340345350																
gct	gcc	aac	ctt	tgg	cca	agc	ccg	ctc	atg	atc	aaa	cgc	tct	aag	aag	1104
Ala	Ala	Asn	Leu	Trp	Pro	Ser	Pro	Leu	Met	Ile	Lys	Arg	Ser	Lys	Lys	
355360365																
aac	agc	ctg	gcc	ttg	tcc	ctg	acg	gcc	gac	cag	atg	gtc	agt	gcc	ttg	1152
Asn	Ser	Leu	Ala	Leu	Ser	Leu	Thr	Ala	Asp	Gln	Met	Val	Ser	Ala	Leu	
370375380																
ttg	gat	gct	gag	ccc	ccc	ata	ctc	tat	tcc	gag	tat	gat	cct	acc	aga	1200
Leu	Asp	Ala	Glu	Pro	Pro	Ile	Leu	Tyr	Ser	Glu	Tyr	Asp	Pro	Thr	Arg	
385390395400																
ccc	ttc	agt	gaa	gct	tcg	atg	atg	ggc	tta	ctg	acc	aac	ctg	gca	gac	1248
Pro	Phe	Ser	Glu	Ala	Ser	Met	Met	Gly	Leu	Leu	Thr	Asn	Leu	Ala	Asp	
405410415																

agg	gag	ctg	gtt	cac	atg	atc	aac	tgg	gcg	aag	agg	gtg	cca	ggc	ttt	1296
Arg	Glu	Leu	Val	His	Met	Ile	Asn	Trp	Ala	Lys	Arg	Val	Pro	Gly	Phe	
			420					425					430			
gtg	gat	ttg	acc	ctc	cat	gat	cag	gtc	cac	ctt	cta	gaa	tgt	gcc	tgg	1344
Val	Asp	Leu	Thr	Leu	His	Asp	Gln	Val	His	Leu	Leu	Glu	Cys	Ala	Trp	
		435					440					445				
cta	gag	atc	ctg	atg	att	ggg	ctc	gtc	tgg	cgc	tcc	atg	gag	cac	cca	1392
Leu	Glu	Ile	Leu	Met	Ile	Gly	Leu	Val	Trp	Arg	Ser	Met	Glu	His	Pro	
	450					455					460					
gtg	aag	cta	ctg	ttt	gct	cct	aac	ttg	ctc	ttg	gac	agg	aac	cag	gga	1440
Val	Lys	Leu	Leu	Phe	Ala	Pro	Asn	Leu	Leu	Leu	Asp	Arg	Asn	Gln	Gly	
465					470					475					480	
aaa	tgt	gta	gag	ggc	atg	gtg	gag	atc	ttc	gac	atg	ctg	ctg	gct	aca	1488
Lys	Cys	Val	Glu	Gly	Met	Val	Glu	Ile	Phe	Asp	Met	Leu	Leu	Ala	Thr	
			485						490					495		
tca	tct	cgg	ttc	cgc	atg	atg	aat	ctg	cag	gga	gag	gag	ttt	gtg	tgc	1536
Ser	Ser	Arg	Phe	Arg	Met	Met	Asn	Leu	Gln	Gly	Glu	Glu	Phe	Val	Cys	
			500					505					510			
ctc	aaa	tct	att	att	ttg	ctt	aat	tct	gga	gtg	tac	aca	ttt	ctg	tcc	1584
Leu	Lys	Ser	Ile	Ile	Leu	Leu	Asn	Ser	Gly	Val	Tyr	Thr	Phe	Leu	Ser	
		515					520					525				
agc	acc	ctg	aag	tct	ctg	gaa	gag	aag	gac	cat	atc	cac	cga	gtc	ctg	1632
Ser	Thr	Leu	Lys	Ser	Leu	Glu	Glu	Lys	Asp	His	Ile	His	Arg	Val	Leu	
	530					535					540					
gac	aag	atc	aca	gac	act	ttg	atc	cac	ctg	atg	gcc	aag	gca	ggc	ctg	1680
Asp	Lys	Ile	Thr	Asp	Thr	Leu	Ile	His	Leu	Met	Ala	Lys	Ala	Gly	Leu	
545				550						555					560	
acc	ctg	cag	cag	cag	cac	cag	cgg	ctg	gcc	cag	ctc	ctc	ctc	atc	ctc	1728
Thr	Leu	Gln	Gln	Gln	His	Gln	Arg	Leu	Ala	Gln	Leu	Leu	Leu	Ile	Leu	
			565					570						575		
tcc	cac	atc	agg	cac	atg	agt	aac	aaa	ggc	atg	gag	cat	ctg	tac	agc	1776
Ser	His	Ile	Arg	His	Met	Ser	Asn	Lys	Gly	Met	Glu	His	Leu	Tyr	Ser	
		580					585						590			
atg	aag	tgc	aag	aac	gtg	gtg	ccc	ctc	tat	gac	ctg	ctg	ctg	gag	gcg	1824
Met	Lys	Cys	Lys	Asn	Val	Val	Pro	Leu	Tyr	Asp	Leu	Leu	Leu	Glu	Ala	
		595					600					605				
gcg	gac	gcc	cac	cgc	cta	cat	gcg	ccc	act	agc	cgt	gga	ggg	gca	tcc	1872
Ala	Asp	Ala	His	Arg	Leu	His	Ala	Pro	Thr	Ser	Arg	Gly	Gly	Ala	Ser	
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gtg	gag	gag	acg	gac	caa</											

cct gcc aca gct tga  
Pro Ala Thr Ala  
660

<220>  
<223> Description of Artificial Sequence: Chimeric sequence  
Homosapiens-Bacteriophage P1

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Asp	Ala	Thr	Ser	Asp	Glu	Val	Arg	Lys	Asn	Leu	Met	Asp	Met	Phe	Arg
			20					25					30		
Asp	Arg	Gln	Ala	Phe	Ser	Glu	His	Thr	Trp	Lys	Met	Leu	Leu	Ser	Val
		35					40					45			
Cys	Arg	Ser	Trp	Ala	Ala	Trp	Cys	Lys	Leu	Asn	Asn	Arg	Lys	Trp	Phe
	50					55					60				
Pro	Ala	Glu	Pro	Glu	Asp	Val	Arg	Asp	Tyr	Leu	Leu	Tyr	Leu	Gln	Ala
65					70					75					80
Arg	Gly	Leu	Ala	Val	Lys	Thr	Ile	Gln	Gln	His	Leu	Gly	Gln	Leu	Asn
				85					90					95	
Met	Leu	His	Arg	Arg	Ser	Gly	Leu	Pro	Arg	Pro	Ser	Asp	Ser	Asn	Ala
			100					105					110		
Val	Ser	Leu	Val	Met	Arg	Arg	Ile	Arg	Lys	Glu	Asn	Val	Asp	Ala	Gly
		115					120					125			
Glu	Arg	Ala	Lys	Gln	Ala	Leu	Ala	Phe	Glu	Arg	Thr	Asp	Phe	Asp	Gln
	130					135					140				
Val	Arg	Ser	Leu	Met	Glu	Asn	Ser	Asp	Arg	Cys	Gln	Asp	Ile	Arg	Asn
145					150					155					160
Leu	Ala	Phe	Leu	Gly	Ile	Ala	Tyr	Asn	Thr	Leu	Leu	Arg	Ile	Ala	Glu
				165					170					175	
Ile	Ala	Arg	Ile	Arg	Val	Lys	Asp	Ile	Ser	Arg	Thr	Asp	Gly	Gly	Arg
			180					185					190		
Met	Leu	Ile	His	Ile	Gly	Arg	Thr	Lys	Thr	Leu	Val	Ser	Thr	Ala	Gly
		195					200								

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp  
 210 215 220  
 Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys  
 225 230 235 240  
 Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu  
 245 250 255  
 Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile  
 260 265 270  
 Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly  
 275 280 285  
 His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val  
 290 295 300  
 Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile  
 305 310 315 320  
 Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val  
 325 330 335  
 Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg  
 340 345 350  
 Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys  
 355 360 365  
 Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu  
 370 375 380  
 Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg  
 385 390 395 400  
 Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp  
 405 410 415  
 Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe  
 420 425 430  
 Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp  
 435 440 445  
 Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro  
 450 455 460  
 Val Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly  
 465 470 475 480  
 Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr  
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 Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys  
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0953033-080801



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<210> 7
<211> 1983
<212> DNA
<213> Artificial sequence
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<220>  
<223> Description of Artificial Sequence: Chimeric sequence  
Homosapiens-Bacteriophage P1

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Met	Ser	Asn	Leu	Leu	Thr	Val	His	Gln	Asn	Leu	Pro	Ala	Leu	Pro	Val	
1		5			10					15						
gat	gca	acg	agt	gat	gag	gtt	cgc	aag	aac	ctg	atg	gac	atg	ttc	agg	96
Asp	Ala	Thr	Ser	Asp	Glu	Val	Arg	Lys	Asn	Leu	Met	Asp	Met	Phe	Arg	
			20		25				30							
gat	cgc	cag	gcg	ttt	tct	gag	cat	acc	tgg	aaa	atg	ctt	ctg	tcc	gtt	144
Asp	Arg	Gln	Ala	Phe	Ser	Glu	His	Thr	Trp	Lys	Met	Leu	Leu	Ser	Val	
		35			40				45							

tgc	cgg	tcg	tgg	gcg	gca	tgg	tgc	aag	ttg	aat	asn	cgg	aaa	tgg	ttt	192
Cys	Arg	Ser	Trp	Ala	Ala	Trp	Cys	Lys	Leu	Asn	Asn	Arg	Lys	Trp	Phe	
505560																
ccc	gca	gaa	cct	gaa	gat	gtt	cgc	gat	tat	ctt	cta	tat	ctt	cag	gcg	240
Pro	Ala	Glu	Pro	Glu	Asp	Val	Arg	Asp	Tyr	Leu	Leu	Tyr	Leu	Gln	Ala	
65707580																
cgc	ggg	ctg	gca	gta	aaa	act	atc	cag	caa	cat	ttg	ggc	cag	cta	aac	288
Arg	Gly	Leu	Ala	Val	Lys	Thr	Ile	Gln	Gln	His	Leu	Gly	Gln	Leu	Asn	
859095																
atg	ctt	cat	cgt	cgg	tcc	ggg	ctg	cca	cga	cca	agt	gac	agc	aat	gct	336
Met	Leu	His	Arg	Arg	Ser	Gly	Leu	Pro	Arg	Pro	Ser	Asp	Ser	Asn	Ala	
100105110																
gtt	tca	ctg	gtt	atg	cgg	cgg	atc	cga	aaa	gaa	aac	gtt	gat	gcc	ggg	384
Val	Ser	Leu	Val	Met	Arg	Arg	Ile	Arg	Lys	Glu	Asn	Val	Asp	Ala	Gly	
115120125																
gaa	cgt	gca	aaa	cag	gct	cta	gcg	ttc	gaa	cgc	act	gat	ttc	gac	cag	432
Glu	Arg	Ala	Lys	Gln	Ala	Leu	Ala	Phe	Glu	Arg	Thr	Asp	Phe	Asp	Gln	
130135140																
gtt	cgt	tca	ctc	atg	gaa	aat	agc	gat	cgc	tgc	cag	gat	ata	cgt	aat	480
Val	Arg	Ser	Leu	Met	Glu	Asn	Ser	Asp	Arg	Cys	Gln	Asp	Ile	Arg	Asn	
145150155																
ctg	gca	ttt	ctg	ggg	att	gct	tat	aac	acc	ctg	tta	cgt	ata	gcc	gaa	528
Leu	Ala	Phe	Leu	Gly	Ile	Ala	Tyr	Asn	Thr	Leu	Leu	Arg	Ile	Ala	Glu	
165170175																
att	gcc	agg	atc	agg	gtt	aaa	gat	atc	tca	cgt	act	gac	ggg	ggg	aga	576
Ile	Ala	Arg	Ile	Arg	Val	Lys	Asp	Ile	Ser	Arg	Thr	Asp	Gly	Gly	Arg	
180185190																
atg	tta	atc	cat	att	ggc	aga	acg	aaa	acg	ctg	gtt	agc	acc	gca	ggg	624
Met	Leu	Ile	His	Ile	Gly	Arg	Thr	Lys	Thr	Leu	Val	Ser	Thr	Ala	Gly	
195200205																
gta	gag	aag	gca	ctt	agc	ctg	ggg	gta	act	aaa	ctg	gtc	gag	cga	tgg	672
Val	Glu	Lys	Ala	Leu	Ser	Leu	Gly	Val	Thr	Lys	Leu	Val	Glu	Arg	Trp	
210215220																
att	tcc	gtc	tct	ggg	gta	gct	gat	gat	cgc	aat	aac	tac	ctg	ttt	tgc	720
Ile	Ser	Val	Ser	Gly	Val	Ala	Asp	Asp	Pro	Asn	Asn	Tyr	Leu	Phe	Cys	
225230235240																
cgg	gtc	aga	aaa	aat	ggg	gtt	gcc	gcg	cca	tct	gcc	acc	agc	cag	cta	768
Arg	Val	Arg	Lys	Asn	Gly	Val	Ala	Ala	Pro	Ser	Ala	Thr	Ser	Gln	Leu	
245250255																
tca	act	cgc	gcc	ctg	gaa	ggg	att	ttt	gaa	gca	act	cat	cga	ttg	att	816
Ser	Thr	Arg	Ala	Leu	Glu	Gly	Ile	Phe	Glu	Ala	Thr	His	Arg	Leu	Ile	
260265270																

tac ggc gct aag gat gac tct ggt cag aga tac ctg gcc tgg tct gga	864
Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly	
275 280 285	
cac agt gcc cgt gtc gga gcc gcg cga gat atg gcc cgc gct gga gtt	912
His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val	
290 295 300	
tca ata ccg gag atc atg caa gct ggt ggc tgg acc aat gta aat att	960
Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile	
305 310 315 320	
gtc atg aac tat atc cgt aac ctg gat agt gaa aca ggg gca atg gtg	1008
Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val	
325 330 335	
cgc ctg ctg gaa gat ggc gat ctc gag cca tct gct gga gac atg aga	1056
Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg	
340 345 350	
gct gcc aac ctt tgg cca agc ccg ctc atg atc aaa cgc tct aag aag	1104
Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys	
355 360 365	
aac agc ctg gcc ttg tcc ctg acg gcc gac cag atg gtc agt gcc ttg	1152
Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu	
370 375 380	
ttg gat gct gag ccc ccc ata ctc tat tcc gag tat gat cct acc aga	1200
Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg	
385 390 395 400	
ccc ttc agt gaa gct tcg atg atg ggc tta ctg acc aac ctg gca gac	1248
Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp	
405 410 415	
agg gag ctg gtt cac atg atc aac tgg gcg aag agg gtg cca ggc ttt	1296
Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe	
420 425 430	
gtg gat ttg acc ctc cat gat cag gtc cac ctt cta gaa tgt gcc tgg	1344
Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp	
435 440 445	
cta gag atc ctg atg att ggt ctc gtc tgg cgc tcc atg gag cac cca	1392
Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro	
450 455 460	
ggg aag cta ctg ttt gct cct aac ttg ctc ttg gac agg aac cag gga	1440
Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly	
465 470 475 480	
aaa tgt gta gag ggc atg gtg gag atc ttc gac atg ctg ctg gct aca	1488
Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr	
485 490 495	

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Asp	Arg	Gln	Ala	Phe	Ser	Glu	His	Thr	Trp	Lys	Met	Leu	Leu	Ser	Val	
			35					40					45			
Cys	Arg	Ser	Trp	Ala	Ala	Trp	Cys	Lys	Leu	Asn	Asn	Arg	Lys	Trp	Phe	
		50					55					60				
Pro	Ala	Glu	Pro	Glu	Asp	Val	Arg	Asp	Tyr	Leu	Leu	Tyr	Leu	Gln	Ala	
		65					70					75		80		
Arg	Gly	Leu	Ala	Val	Lys	Thr	Ile	Gln	Gln	His	Leu	Gly	Gln	Leu	Asn	
			85					90					95			
Met	Leu	His	Arg	Arg	Ser	Gly	Leu	Pro	Arg	Pro	Ser	Asp	Ser	Asn	Ala	
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Val	Ser	Leu	Val	Met	Arg	Arg	Ile	Arg	Lys	Glu	Asn	Val	Asp	Ala	Gly	
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Glu	Arg	Ala	Lys	Gln	Ala	Leu	Ala	Phe	Glu	Arg	Thr	Asp	Phe	Asp	Gln	
		130					135					140				
Val	Arg	Ser	Leu	Met	Glu	Asn	Ser	Asp	Arg	Cys	Gln	Asp	Ile	Arg	Asn	
		145					150					155		160		
Leu	Ala	Phe	Leu	Gly	Ile	Ala	Tyr	Asn	Thr	Leu	Leu	Arg	Ile	Ala	Glu	
			165					170					175			
Ile	Ala	Arg	Ile	Arg	Val	Lys	Asp	Ile	Ser	Arg	Thr	Asp	Gly	Gly	Arg	
			180					185					190			
Met	Leu	Ile	His	Ile	Gly	Arg	Thr	Lys	Thr	Leu	Val	Ser	Thr	Ala	Gly	
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Val	Glu	Lys	Ala	Leu	Ser	Leu	Gly	Val	Thr	Lys	Leu	Val	Glu	Arg	Trp	
		210					215					220				
Ile	Ser	Val	Ser	Gly	Val	Ala	Asp	Asp	Pro	Asn	Asn	Tyr	Leu	Phe	Cys	
		225					230					235		240		
Arg	Val	Arg	Lys	Asn	Gly	Val	Ala	Ala	Pro	Ser	Ala	Thr	Ser	Gln	Leu	
			245					250					255			
Ser	Thr	Arg	Ala	Leu	Glu	Gly	Ile	Phe	Glu	Ala	Thr	His	Arg	Leu	Ile	
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Tyr	Gly	Ala	Lys	Asp	Asp	Ser	Gly	Gln	Arg	Tyr	Leu	Ala	Trp	Ser	Gly	
		275					280					285				
His	Ser	Ala	Arg	Val	Gly	Ala	Ala	Arg	Asp	Met	Ala	Arg	Ala	Gly	Val	
		290					295					300				
Ser	Ile	Pro	Glu	Ile	Met	Gln	Ala	Gly	Gly	Trp	Thr	Asn	Val	Asn	Ile	
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Val	Met	Asn	Tyr	Ile	Arg	Asn	Leu	Asp	Ser	Glu	Thr	Gly	Ala	Met	Val	
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				340					345					350		
Ala	Ala	Asn	Leu	Trp	Pro	Ser	Pro	Leu	Met	Ile	Lys	Arg	Ser	Lys	Lys	
				355					360					365		
Asn	Ser	Leu	Ala	Leu	Ser	Leu	Thr	Ala	Asp	Gln	Met	Val	Ser	Ala	Leu	
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Leu	Asp	Ala	Glu	Pro	Pro	Ile	Leu	Tyr	Ser	Glu	Tyr	Asp	Pro	Thr	Arg	
				385					390					395		
Pro	Phe	Ser	Glu	Ala	Ser	Met	Met	Gly	Leu	Leu	Thr	Asn	Leu	Ala	Asp	
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Arg	Glu	Leu	Val	His	Met	Ile	Asn	Trp	Ala	Lys	Arg	Val	Pro	Gly	Phe	
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Val	Asp	Leu	Thr	Leu	His	Asp	Gln	Val	His	Leu	Leu	Glu	Cys	Ala	Trp	
				435					440					445		
Leu	Glu	Ile	Leu	Met	Ile	Gly	Leu	Val	Trp	Arg	Ser	Met	Glu	His	Pro	
				450					455					460		
Gly	Lys	Leu	Leu	Phe	Ala	Pro	Asn	Leu	Leu	Leu	Asp	Arg	Asn	Gln	Gly	
				465					470					475		
Lys	Cys	Val	Glu	Gly	Met	Val	Glu	Ile	Phe	Asp	Met	Leu	Leu	Ala	Thr	
				485					490					495		
Ser	Ser	Arg	Phe	Arg	Met	Met	Asn	Leu	Gln	Gly	Glu	Glu	Phe	Val	Cys	
				500					505					510		
Leu	Lys	Ser	Ile	Ile	Leu	Leu	Asn	Ser	Gly	Val	Tyr	Thr	Phe	Leu	Ser	
				515					520					525		
Ser	Thr	Leu	Lys	Ser	Leu	Glu	Glu	Lys	Asp	His	Ile	His	Arg	Val	Leu	
				530					535					540		
Asp	Lys	Ile	Thr	Asp	Thr	Leu	Ile	His	Leu	Met	Ala	Lys	Ala	Gly	Leu	
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Thr	Leu	Gln	Gln	Gln	His	Gln	Arg	Leu	Ala	Gln	Leu	Leu	Leu	Ile	Leu	
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Ser	His	Ile	Arg	His	Met	Ser	Asn	Lys	Gly	Met	Glu	His	Leu	Tyr	Ser	
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Met	Lys	Cys	Lys	Asn	Val	Val	Pro	Leu	Tyr	Asp	Leu	Leu	Leu	Glu	Ala	
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Ala	Asp	Ala	His	Arg	Leu	His	Ala	Pro	Thr	Ser	Arg	Gly	Gly	Ala	Ser	
				610					615					620		

Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser  
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